Please replace the paragraph beginning at page 15, line 1, with the following rewritten paragraph:

This same assay, combining a sample with the nucleotide sequence, is applicable in evaluating the efficacy of a particular therapeutic treatment regime. It may be used in animal studies, in clinical trials, or in monitoring the treatment of an individual patient. First, standard expression must be established for use as a basis of comparison. Second, samples from the animals or patients affected by a disorder or disease are combined with the nucleotide sequence to evaluate the deviation from the standard or normal profile. Third, an entirely new or pre-existing therapeutic agent is administered, and a treatment profile is generated. This post-treatment assay is evaluated to determine whether the patient profile progresses toward or returns to the standard pattern. Successive treatment profiles may be used to show the efficacy of treatment over a period of several days or several months.

D2

Please replace the paragraph beginning at page 17, line 32 and ending on page 18, line 6, with the following rewritten paragraph:

The cDNA library was constructed from normal placenta. The tissue was lysed in a buffer containing guanidinium isothiocyanate. The lysate was extracted with phenol chloroform and precipitated with ethanol. Poly A^+ RNA was isolated using biotinylated oligo d(T) primer and streptavidin coupled to a paramagnetic particle (Promega Corp. Madison WI) and sent to Stratagene (La Jolla CA) for cDNA library preparation. The cDNA synthesis was primed using both oligo d(T) and random hexamers, and the two cDNA libraries were treated separately. Synthetic adapter oligonucleotides were ligated onto the ends of the cDNAs which were digested with XhoI and inserted into the UNIZAP vector system (Stratagene).

D3

Please replace the paragraph beginning at page 23, line 11 with the following rewritten paragraph:

Knowledge of the correct cDNA sequence of this Jak2 kinase or its regulatory elements enable its use as a tool in sense (Youssoufian H and HF Lodish 1993) Mol Cell Biol 13:98-104) or antisense (Eguchi et al (1991) Annu Rev Biochem 60:631-652) technologies for the investigation or alteration of gene expression. To inhibit in vivo or in vitro hjak2 expression, an

D4

oligonucleotide based on the coding sequence of an hjak2 designed with OLIGO 4.0 software (National Biosciences Inc) is used. Alternatively, a fragment of an hjak2 is produced by digesting hjak2 coding sequence with restriction enzymes. These enzymes and specific restrictions sites may be selected using INHERIT analysis software (Applied Biosystems), and the strands separated by heating the fragments and selecting for the antisense strand. Either the oligonucleotide or the fragment may be used to inhibit hjak2 expression. Furthermore, antisense molecules can be designed to inhibit promoter binding in the upstream nontranslated leader or at various sites along the hjak2 coding region. Alternatively, antisense molecules may be designed to inhibit translation of an mRNA into polypeptide by preparing an oligomer or fragment which will bind in the region spanning approximately -10 to +10 nucleotides at the 5' end of the coding sequence. These technologies are now well known to those of in the art.

Please replace the paragraph beginning at page 26, line 18 with the following rewritten paragraph:

The sequence for HJAK2 in this application present many different domains (and subdomains as detailed in the background of the invention) which may be utilized: 1) individually for the production of antibodies, 2) in functional groups (eg. to span a membrane), and 3) as interchangeable, usable parts of a chimeric kinase. For example, a known, full length kinase such as the hjak2 kinase of this application may be used to swap related portions of the nucleic acid sequence, analogous to domains or subdomains of MAP kinase polypeptides. The chimeric nucleotides, so produced, may be introduced into prokaryotic host cells (as reviewed in Strosberg AD and Marullo S (1992) Trends Pharma Sci 13:95-98) or eukaryotic host cells. These host cells are then employed in procedures to determine what molecules activate the kinase or what molecules are activated by a kinase. Such activating or activated molecules may be of extracellular, intracellular, biologic or chemical origin.

Please replace the paragraph beginning at page 30, line 2 with the following rewritten paragraph:

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia Biotech). Likewise,